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calculated values with experimental inhibition constants K_i of the compounds was developed. The success of the calculations was evaluated by the consistency of the calculated free energy changes of binding and the experimental K_i.

IN THE ABSTRACT:

Please replace the abstract with the following abstract (a marked-up copy of the amended abstract is attached to this Amendment):

Please replace the paragraph on page 51, lines 1-12, with the following paragraph.

ABSTRACT OF THE DISCLOSURE

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Provided herein are computer-based methods for generating and using three-dimensional (3-D) structural models of target biomolecules. In particular, the target biomolecules are protein structural variants derived from genes containing genetic variations, or polymorphisms. The models are generated using molecular modeling techniques, such as homology modeling. The models can be used in structure-based drug design studies to identify drugs that bind to particular structural variants in structure-based drug design studies, for designing allele-specific drugs, population-specific drugs and for predicting clinical responses in patients. Molecular structure databases containing protein structural variant models are also provided.

IN THE CLAIMS:

Please cancel claims 1-22 and 24-40 without prejudice or disclaimer.

REMARKS

A check in the amount of $1440.00 for a four-month extension of time (large entity) is enclosed. Any fees that may be due in connection with this paper, or with this application throughout its pendency, may be charged to Deposit Account No. 50-1213. If a Petition for an Extension of Time in required, this paper is to be considered such Petition.